

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/830, 837B

Source: IFW16

Date Processed by STIC: 2/23/06

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 09/830,837B

CRF Edit Date: 2/23/06
Edited by: AK

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

✓ Corrected the SEQ ID NO. Sequence numbers edited were:
61,87

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

✓ Deleted: ✓ invalid beginning/end-of-file text ; ___ page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

___ Moved responses to same line as heading/numeric identifier, specifically:

___ Other:



IFW16

RAW SEQUENCE LISTING

DATE: 02/24/2006

PATENT APPLICATION: US/09/830,837B

TIME: 15:45:00

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\02242006\I830837B.raw

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3 <110> APPLICANT: Institut de Recherches Cliniques de Montreal
4     Seidah, Nabil
5     ChrEtien, Michel
6     Marcinkiewicz, Mieczyslaw
7     Laaksonen, Reijo
8     Davignon, Jean
10 <120> TITLE OF INVENTION: MAMMALIAN SUBTILISIN/KEXIN ISOZYME SKI-1: A PROPROTEIN
CONVERTASE
11     WITH A UNIQUE CLEAVAGE SPECIFICITY
13 <130> FILE REFERENCE: 10992.29
15 <140> CURRENT APPLICATION NUMBER: US 09/830,837B
C--> 16 <141> CURRENT FILING DATE: 2001-10-18
18 <150> PRIOR APPLICATION NUMBER: PCT/CA1999/01058
19 <151> PRIOR FILING DATE: 1999-11-04
21 <150> PRIOR APPLICATION NUMBER: CA 2,249,648
22 <151> PRIOR FILING DATE: 1998-11-04
24 <160> NUMBER OF SEQ ID NOS: 108
26 <170> SOFTWARE: PatentIn version 3.3
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29 <211> LENGTH: 3895
30 <212> TYPE: DNA
31 <213> ORGANISM: Rattus sp.
34 <220> FEATURE:
35 <221> NAME/KEY: CDS
36 <222> LOCATION: (418)..(3573)
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43 tcctgctaga tttgggtctg tggtaacaaat ggagtttagg actcagtgga ctcggcccta      180
45 atgagagaag cccctgtcc aagatggaga agaagcggag aaagaaatga aagcctcttt      240
47 ttgggccaa gctgtgggtga ccatgggact gaggttttct ttacgttgga caagtctgta      300
49 ggatggctga tcagtaagg tgcagctttt agcgaaaaca gaaatccact tctgatcaag      360
51 gaagagccta gtgcaatttg aatttatgca attttatgac catattcact taggacc          417
53 atg aag ctc gtc aac atc tgg ctt ctt ctg ctg gtg gtt ttg ctc tgt          465
54 Met Lys Leu Val Asn Ile Trp Leu Leu Leu Leu Val Val Leu Leu Cys
55 1             5             10             15
57 ggg aaa aag cat ctg ggt gac agg ctg ggg aag aaa gct ttt gaa aag          513
58 Gly Lys Lys His Leu Gly Asp Arg Leu Gly Lys Lys Ala Phe Glu Lys
59             20             25             30
61 gcc cca tgc ccc agc tgt tcc cac ctg act ttg aag gtg gaa ttc tcc          561
62 Ala Pro Cys Pro Ser Cys Ser His Leu Thr Leu Lys Val Glu Phe Ser
63             35             40             45
65 tca act gtg gtg gaa tat gaa tat att gtg gct ttc aac gga tac ttc          609
66 Ser Thr Val Val Glu Tyr Glu Tyr Ile Val Ala Phe Asn Gly Tyr Phe

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Input Set : A:\PTO.AMC.txt

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67	50	55	60	
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70	Thr Ala Lys Ala Arg Asn Ser Phe Ile Ser Ser Ala Leu Lys Ser Ser			
71	65 70 75 80			
73	gaa gtg gac aac tgg aga ata ata cct cgg aac aac cca tct agt gac	705		
74	Glu Val Asp Asn Trp Arg Ile Ile Pro Arg Asn Asn Pro Ser Ser Asp			
75	85 90 95			
77	tac cct agt gat ttt gag gtg att cag ata aaa gag aag cag aag gcg	753		
78	Tyr Pro Ser Asp Phe Glu Val Ile Gln Ile Lys Glu Lys Gln Lys Ala			
79	100 105 110			
81	ggg ctg ctc aca ctt gaa gat cac cca aac atc aag cgg gtg aca ccc	801		
82	Gly Leu Leu Thr Leu Glu Asp His Pro Asn Ile Lys Arg Val Thr Pro			
83	115 120 125			
85	cag cgg aaa gtc ttt cgt tcc ctg aag ttt gct gaa tcc gac ccc att	849		
86	Gln Arg Lys Val Phe Arg Ser Leu Lys Phe Ala Glu Ser Asp Pro Ile			
87	130 135 140			
89	gtg ccc tgt aat gag acc cgg tgg agc cag aag tgg cag tca tca cgt	897		
90	Val Pro Cys Asn Glu Thr Arg Trp Ser Gln Lys Trp Gln Ser Ser Arg			
91	145 150 155 160			
93	ccc ctg aaa aga gcc agt ctc tcc ctg ggc tct gga ttc tgg cat gca	945		
94	Pro Leu Lys Arg Ala Ser Leu Ser Leu Gly Ser Gly Phe Trp His Ala			
95	165 170 175			
97	aca gga agg cat tca agt cga cga ttg ctg aga gcc att cct cgc cag	993		
98	Thr Gly Arg His Ser Ser Arg Arg Leu Leu Arg Ala Ile Pro Arg Gln			
99	180 185 190			
101	gtt gcc cag aca ttg cag gca gat gtg ctt tgg cag atg gga tac aca	1041		
102	Val Ala Gln Thr Leu Gln Ala Asp Val Leu Trp Gln Met Gly Tyr Thr			
103	195 200 205			
105	ggt gct aat gtc agg gtt gcc gtt ttt gat act ggg ctc agt gag aag	1089		
106	Gly Ala Asn Val Arg Val Ala Val Phe Asp Thr Gly Leu Ser Glu Lys			
107	210 215 220			
109	cat cca cat ttc aag aat gtg aag gaa aga acc aac tgg acc aat gag	1137		
110	His Pro His Phe Lys Asn Val Lys Glu Arg Thr Asn Trp Thr Asn Glu			
111	225 230 235 240			
113	cgg acc ctg gac gat ggg ctg ggc cat ggc aca ttc gtt gca ggt gtg	1185		
114	Arg Thr Leu Asp Asp Gly Leu Gly His Gly Thr Phe Val Ala Gly Val			
115	245 250 255			
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120	Ile Ala Ser Met Arg Glu Cys Gln Gly Phe Ala Pro Asp Ala Glu Leu			
121	260 265 270			
123	cac atc ttc agg gtc ttt acc aac aat cag gtg tct tac acg tct tgg	1281		
124	His Ile Phe Arg Val Phe Thr Asn Asn Gln Val Ser Tyr Thr Ser Trp			
125	275 280 285			
127	ttt ttg gat gcc ttc aac tat gcc atc cta aag aag atg gac gtt ctg	1329		
128	Phe Leu Asp Ala Phe Asn Tyr Ala Ile Leu Lys Lys Met Asp Val Leu			
129	290 295 300			
131	aac ctt agc atc ggt ggg cct gac ttc atg gat cac ccc ttt gtt gac	1377		
132	Asn Leu Ser Ile Gly Pro Asp Phe Met Asp His Pro Phe Val Asp			
133	305 310 315 320			

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136	Lys Val Trp Glu Leu Thr Ala Asn Asn Val Ile Met Val Ser Ala Ile	
137	325 330 335	
139	ggc aat gat gga cct ctc tat ggc act ctg aat aac cct gct gat cag	1473
140	Gly Asn Asp Gly Pro Leu Tyr Gly Thr Leu Asn Asn Pro Ala Asp Gln	
141	340 345 350	
143	atg gat gtg att gga gtg ggt ggc att gac ttt gaa gac aac atc gcc	1521
144	Met Asp Val Ile Gly Val Gly Gly Ile Asp Phe Glu Asp Asn Ile Ala	
145	355 360 365	
147	cgc ttc tct tcc agg gga atg act acc tgg gaa cta ccg gga ggc tat	1569
148	Arg Phe Ser Ser Arg Gly Met Thr Thr Trp Glu Leu Pro Gly Gly Tyr	
149	370 375 380	
151	ggg cgt gtg aag cct gac att gtc acc tat ggt gct gga gtg cgg ggt	1617
152	Gly Arg Val Lys Pro Asp Ile Val Thr Tyr Gly Ala Gly Val Arg Gly	
153	385 390 395 400	
155	tct ggt gtg aaa ggg ggc tgc cgt gca ctc tca ggg acc agt gtc gcc	1665
156	Ser Gly Val Lys Gly Gly Cys Arg Ala Leu Ser Gly Thr Ser Val Ala	
157	405 410 415	
159	tcc cca gtg gtt gct ggg gct gtc acc ttg tta gta agc aca gta cag	1713
160	Ser Pro Val Val Ala Gly Ala Val Thr Leu Leu Val Ser Thr Val Gln	
161	420 425 430	
163	aag cgg gag cta gtg aat cct gcc agt gtg aag caa gct ttg ata gca	1761
164	Lys Arg Glu Leu Val Asn Pro Ala Ser Val Lys Gln Ala Leu Ile Ala	
165	435 440 445	
167	tca gcc cgg aga ctt cct ggt gtc aac atg ttt gag caa ggc cat ggc	1809
168	Ser Ala Arg Arg Leu Pro Gly Val Asn Met Phe Glu Gln Gly His Gly	
169	450 455 460	
171	aag ttg gat cta ctg cga gcc tat cag atc ctc agc agc tat aaa ccg	1857
172	Lys Leu Asp Leu Leu Arg Ala Tyr Gln Ile Leu Ser Ser Tyr Lys Pro	
173	465 470 475 480	
175	cag gcg agc ctg agt cct agc tac atc gac ctg act gag tgt ccc tac	1905
176	Gln Ala Ser Leu Ser Pro Ser Tyr Ile Asp Leu Thr Glu Cys Pro Tyr	
177	485 490 495	
179	atg tgg ccc tac tgc tcc cag ccc atc tac tat gga gga atg cca aca	1953
180	Met Trp Pro Tyr Cys Ser Gln Pro Ile Tyr Tyr Gly Gly Met Pro Thr	
181	500 505 510	
183	att gtt aat gtc acc atc ctc aat ggc atg gga gtt aca gga aga att	2001
184	Ile Val Asn Val Thr Ile Leu Asn Gly Met Gly Val Thr Gly Arg Ile	
185	515 520 525	
187	gtg gat aag cct gag tgg cga ccc tat tta cca cag aat gga gac aac	2049
188	Val Asp Lys Pro Glu Trp Arg Pro Tyr Leu Pro Gln Asn Gly Asp Asn	
189	530 535 540	
191	att gaa gtg gcc ttc tcc tac tcc tca gtg ttg tgg cct tgg tca ggt	2097
192	Ile Glu Val Ala Phe Ser Tyr Ser Ser Val Leu Trp Pro Trp Ser Gly	
193	545 550 555 560	
195	tac ctt gcc atc tcc att tct gtg acc aag aag gca gct tcc tgg gaa	2145
196	Tyr Leu Ala Ile Ser Ile Ser Val Thr Lys Lys Ala Ala Ser Trp Glu	
197	565 570 575	
199	ggc atc gcg cag ggc cac atc atg atc aca gtg gct tcc cca gca gag	2193

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201				580					585					590			
203	acg	gaa	tta	aaa	aat	ggt	gcc	gag	cat	act	tcc	aca	gtg	aag	ctg	ccc	2241
204	Thr	Glu	Leu	Lys	Asn	Gly	Ala	Glu	His	Thr	Ser	Thr	Val	Lys	Leu	Pro	
205				595				600					605				
207	atc	aag	gtg	aag	atc	att	ccc	acc	cct	cct	cgg	agc	aag	aga	gtc	ctc	2289
208	Ile	Lys	Val	Lys	Ile	Ile	Pro	Thr	Pro	Pro	Arg	Ser	Lys	Arg	Val	Leu	
209				610				615					620				
211	tgg	gac	cag	tac	cac	aac	ctc	cgc	tac	cca	ccc	ggc	tac	ttc	ccc	agg	2337
212	Trp	Asp	Gln	Tyr	His	Asn	Leu	Arg	Tyr	Pro	Pro	Gly	Tyr	Phe	Pro	Arg	
213	625					630						635				640	
215	gac	aac	ttg	cgg	atg	aag	aat	gat	cct	tta	gac	tgg	aat	ggc	gac	cac	2385
216	Asp	Asn	Leu	Arg	Met	Lys	Asn	Asp	Pro	Leu	Asp	Trp	Asn	Gly	Asp	His	
217						645						650				655	
219	gtc	cac	acc	aac	ttc	agg	gac	atg	tac	cag	cat	ctg	cgc	agc	atg	ggc	2433
220	Val	His	Thr	Asn	Phe	Arg	Asp	Met	Tyr	Gln	His	Leu	Arg	Ser	Met	Gly	
221				660								665				670	
223	tac	ttt	gtg	gag	gtg	ctt	ggt	gcc	cca	ttc	aca	tgc	ttt	gac	gcc	acg	2481
224	Tyr	Phe	Val	Glu	Val	Leu	Gly	Ala	Pro	Phe	Thr	Cys	Phe	Asp	Ala	Thr	
225				675				680					685				
227	cag	tac	ggc	act	ctg	ctt	atg	gtg	gac	agt	gag	gaa	gag	tac	ttc	cct	2529
228	Gln	Tyr	Gly	Thr	Leu	Leu	Met	Val	Asp	Ser	Glu	Glu	Glu	Tyr	Phe	Pro	
229				690				695					700				
231	gag	gag	att	gct	aag	ctg	agg	agg	gac	gtg	gac	aat	ggc	ctt	tcc	ctt	2577
232	Glu	Glu	Ile	Ala	Lys	Leu	Arg	Arg	Asp	Val	Asp	Asn	Gly	Leu	Ser	Leu	
233	705					710						715				720	
237	gtc	gtc	ttc	agt	gac	tgg	tac	aac	act	tct	ggt	atg	aga	aaa	gtg	aag	2625
238	Val	Val	Phe	Ser	Asp	Trp	Tyr	Asn	Thr	Ser	Val	Met	Arg	Lys	Val	Lys	
239						725						730				735	
241	ttt	tac	gat	gaa	aac	aca	agg	cag	tgg	tgg	atg	cca	gat	act	gga	gga	2673
242	Phe	Tyr	Asp	Glu	Asn	Thr	Arg	Gln	Trp	Trp	Met	Pro	Asp	Thr	Gly	Gly	
243				740								745				750	
245	gcc	aac	gtc	cca	gct	cta	aac	gag	ctg	ctg	tct	gtg	tgg	aac	atg	ggg	2721
246	Ala	Asn	Val	Pro	Ala	Leu	Asn	Glu	Leu	Leu	Ser	Val	Trp	Asn	Met	Gly	
247				755				760					765				
249	ttc	agt	gac	ggc	ctg	tat	gaa	ggg	gag	ttt	gcc	ctg	gca	aac	cac	gac	2769
250	Phe	Ser	Asp	Gly	Leu	Tyr	Glu	Gly	Glu	Phe	Ala	Leu	Ala	Asn	His	Asp	
251				770				775					780				
253	atg	tac	tat	gca	tcg	ggg	tgc	agc	att	gcc	agg	ttt	cca	gaa	gat	ggt	2817
254	Met	Tyr	Tyr	Ala	Ser	Gly	Cys	Ser	Ile	Ala	Arg	Phe	Pro	Glu	Asp	Gly	
255	785					790						795				800	
257	gtg	gtg	atc	aca	cag	act	ttc	aag	gac	caa	gga	ttg	gaa	gtc	tta	aaa	2865
258	Val	Val	Ile	Thr	Gln	Thr	Phe	Lys	Asp	Gln	Gly	Leu	Glu	Val	Leu	Lys	
259						805						810				815	
261	caa	gag	aca	gca	ggt	gtc	gac	aat	gtc	ccc	att	ctg	ggg	cta	tat	cag	2913
262	Gln	Glu	Thr	Ala	Val	Val	Asp	Asn	Val	Pro	Ile	Leu	Gly	Leu	Tyr	Gln	
263				820						825						830	
265	att	cca	gct	gaa	ggt	gga	ggc	cgg	att	gtg	ctg	tat	gga	gac	tcc	aac	2961
266	Ile	Pro	Ala	Glu	Gly	Gly	Gly	Arg	Ile	Val	Leu	Tyr	Gly	Asp	Ser	Asn	

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269 tgc ttg gat gac agt cac aga cag aag gac tgc ttt tgg ctt ctg gat      3009
270 Cys Leu Asp Asp Ser His Arg Gln Lys Asp Cys Phe Trp Leu Leu Asp
271      850      855      860
273 gca ctc ctt cag tac aca tcc tat ggt gtg acc cct ccc agc ctc agc      3057
274 Ala Leu Leu Gln Tyr Thr Ser Tyr Gly Val Thr Pro Pro Ser Leu Ser
275 865      870      875      880
277 cat tca ggg aac cgg cag cgc cca ccc agc ggg gct ggc ttg gcc cct      3105
278 His Ser Gly Asn Arg Gln Arg Pro Pro Ser Gly Ala Gly Leu Ala Pro
279      885      890      895
281 cct gaa agg atg gaa gga aac cac ctt cat cgc tac tcc aaa gtt ctt      3153
282 Pro Glu Arg Met Glu Gly Asn His Leu His Arg Tyr Ser Lys Val Leu
283      900      905      910
285 gag gcc cac ttg gga gac ccg aaa cct cgg ccc ctt cca gcc tgt cca      3201
286 Glu Ala His Leu Gly Asp Pro Lys Pro Arg Pro Leu Pro Ala Cys Pro
287      915      920      925
289 cac ttg tgc tgg gcc aag cca cag cct ttg aat gag acg gca ccc agt      3249
290 His Leu Ser Trp Ala Lys Pro Gln Pro Leu Asn Glu Thr Ala Pro Ser
291      930      935      940
293 aat ctt tgg aaa cac cag aag ctg ctc tcc att gac ctg gac aaa gta      3297
294 Asn Leu Trp Lys His Gln Lys Leu Leu Ser Ile Asp Leu Asp Lys Val
295 945      950      955      960
297 gtg tta ccc aac ttt cgc tca aat cgc cct caa gtg aga cct ttg tcc      3345
298 Val Leu Pro Asn Phe Arg Ser Asn Arg Pro Gln Val Arg Pro Leu Ser
299      965      970      975
301 cct gga gaa agt ggt gcc tgg gac att cct gga ggg atc atg cct ggc      3393
302 Pro Gly Glu Ser Gly Ala Trp Asp Ile Pro Gly Gly Ile Met Pro Gly
303      980      985      990
305 cgc tac aac cag gaa gta ggc cag acc atc cct gtt ttt gcc ttc ctt      3441
306 Arg Tyr Asn Gln Glu Val Gly Gln Thr Ile Pro Val Phe Ala Phe Leu
307      995      1000      1005
309 gga gcc atg gtg gcc ctg gcc ttc ttc gtg gta cag atc agt aag      3486
310 Gly Ala Met Val Ala Leu Ala Phe Phe Val Val Gln Ile Ser Lys
311      1010      1015      1020
313 gcc aag agc cgg ccg aag cgg agg agg ccc agg gca aag cgt cca      3531
314 Ala Lys Ser Arg Pro Lys Arg Arg Arg Pro Arg Ala Lys Arg Pro
315      1025      1030      1035
317 caa ctt gca cag cag gcc cac cct gca agg acc ccg tca gtg      3573
318 Gln Leu Ala Gln Gln Ala His Pro Ala Arg Thr Pro Ser Val
319      1040      1045      1050
321 tgatcatcac agtggccaga cacagaagct gacaagcttt gaacccctct ggtggccaca      3633
323 cagcatcaga gagcatcctg ggaagtgcct gtttccaagg agccctatct ctggattgtg      3693
325 gctggcttag tgtgttctgc ccagacgtct atgaggtaca tcctgcagtg cctcactgtg      3753
327 tttggctctg gccgaagggtg ccagtagct cagcctccgg tggcatcagg ccagtgaca      3813
329 gtgcacaaa gacacagagc ctggaagggc tgcggggaca tactttctac ataatgctac      3873
331 aaccctgacc aagcgaagac at      3895
334 <210> SEQ ID NO: 2
335 <211> LENGTH: 1052
336 <212> TYPE: PRT

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; Xaa Pos. 2,3,4,5,6,7
Seq#:8; Xaa Pos. 2,3,4,5,6,7
Seq#:9; Xaa Pos. 2,3,4,5,6,7,8
Seq#:10; Xaa Pos. 2,3,4,5,6,7,8
Seq#:11; Xaa Pos. 2,3,4,5,6,7,8,9
Seq#:12; Xaa Pos. 2,3,4,5,6,7,8,9
Seq#:14; Xaa Pos. 1,13
Seq#:15; N Pos. 3,9,12,18,21
Seq#:16; N Pos. 3,6,9,12,15,18,21,24,29
Seq#:17; Xaa Pos. 5,6
Seq#:18; Xaa Pos. 4,6,8,10
Seq#:46; Xaa Pos. 1,13
Seq#:47; Xaa Pos. 1,11
Seq#:74; Xaa Pos. 1,13
Seq#:75; Xaa Pos. 1,11
Seq#:76; Xaa Pos. 1,14
Seq#:101; Xaa Pos. 1
Seq#:102; Xaa Pos. 1
Seq#:103; Xaa Pos. 6
Seq#:107; Xaa Pos. 1,11

VERIFICATION SUMMARY

DATE: 02/24/2006

PATENT APPLICATION: US/09/830,837B

TIME: 15:45:01

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\02242006\I830837B.raw

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1811 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:1852 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:1887 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:1927 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:1965 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:2005 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:2033 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:2038 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:2044 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:2083 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:2141 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:2165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:2201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:2585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0
L:2610 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47 after pos.:0
L:2928 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74 after pos.:0
L:2953 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75 after pos.:0
L:2978 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:0
L:3279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:101 after pos.:0
L:3299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:102 after pos.:0
L:3319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103 after pos.:0
L:3377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:107 after pos.:0

**Raw Sequence Listing before editing
(for reference only)**



IFW16

RAW SEQUENCE LISTING

DATE: 02/23/2006

PATENT APPLICATION: US/09/830,837B

TIME: 11:44:13

Input Set : A:\PTO.TS.23.txt

Output Set: N:\CRF4\02232006\I830837B.raw

3 <110> APPLICANT: Institut de Recherches Cliniques de Montreal
 4 Seidah, Nabil
 5 ChrEtien, Michel
 6 Marcinkiewicz, Mieczyslaw
 7 Laaksonen, Reijo
 8 Davignon, Jean
 10 <120> TITLE OF INVENTION: MAMMALIAN SUBTILISIN/KEXIN ISOZYME SKI-1: A PROPROTEIN
 CONVERTASE
 11 WITH A UNIQUE CLEAVAGE SPECIFICITY
 13 <130> FILE REFERENCE: 10992.29
 15 <140> CURRENT APPLICATION NUMBER: US 09/830,837B
 C--> 16 <141> CURRENT FILING DATE: 2001-10-18
 18 <150> PRIOR APPLICATION NUMBER: PCT/CA1999/01058
 19 <151> PRIOR FILING DATE: 1999-11-04
 21 <150> PRIOR APPLICATION NUMBER: CA 2,249,648
 22 <151> PRIOR FILING DATE: 1998-11-04
 24 <160> NUMBER OF SEQ ID NOS: 108
 26 <170> SOFTWARE: PatentIn version 3.3

**Does Not Comply
 Corrected Diskette Needed**

ERRORED SEQUENCES

E--> 2757 <210> SEQ ID NO: 64 61
 2758 <211> LENGTH: 16
 2759 <212> TYPE: PRT
 2760 <213> ORGANISM: Bovis sp.
 @K> 2762 <400> SEQUENCE: 61
 2764 Glu Leu Glu Asn Leu Ala Ala Met Asp Leu Glu Leu Gln Lys Ile Ala
 2765 1 5 10 15
 @K> 2768 <210> SEQ ID NO: 62
 3100 <210> SEQ ID NO: 87
 3101 <211> LENGTH: 11
 3102 <212> TYPE: PRT
 3103 <213> ORGANISM: Sus sp.
 E--> 3105 <400> SEQUENCE: 78 87
 3107 Arg Gly Leu Thr Ser Ser Ser Ser Ser Leu
 3108 1 5 10
 3381 <210> SEQ ID NO: 108
 3382 <211> LENGTH: 12
 3383 <212> TYPE: PRT
 3384 <213> ORGANISM: Homo sapiens
 3386 <400> SEQUENCE: 108
 3388 Gln Arg Lys Val Phe Arg Ser Leu Lys Tyr Ala Glu
 3389 1 5 10

P.2

RAW SEQUENCE LISTING

DATE: 02/23/2006

PATENT APPLICATION: US/09/830,837B

TIME: 11:44:13

Input Set : A:\PTO.TS.23.txt

Output Set: N:\CRF4\02232006\I830837B.raw

E--> 3393 58
3396 1/34

VERIFICATION SUMMARY

DATE: 02/23/2006

PATENT APPLICATION: US/09/830,837B

TIME: 11:44:14

Input Set : A:\PTO.TS.23.txt

Output Set: N:\CRF4\02232006\I830837B.raw

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:1811 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
 L:1852 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
 L:1887 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
 L:1927 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
 L:1965 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
 L:2005 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
 L:2033 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
 L:2038 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
 L:2044 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
 L:2083 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
 L:2141 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
 L:2165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
 L:2201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
 L:2585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0
 L:2610 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47 after pos.:0
 L:2757 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 61 thru 63
 L:2762 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:64 differs:61
 L:2768 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 62
 L:2928 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74 after pos.:0
 L:2953 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75 after pos.:0
 L:2978 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:0
 L:3105 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:87 differs:78
 L:3279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:101 after pos.:0
 L:3299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:102 after pos.:0
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 L:3377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:107 after pos.:0
 L:3393 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:108